

Accelerating and Benchmarking GAMESS quantum chemistry code on Mira

Maricris Mayes, Graham D. Fletcher, Yuri Alexeev Argonne National Laboratory Leadership Computing Facility

Mark S. Gordon

Iowa State University



Outline

- Introduction
 - Motivation
 - Overview of ab initio MD and quantum chemistry
 - GAMESS
 - Fragment Molecular Orbital
- Performance on Mira
- What is enabled by Mira over Intrepid?
- Code Modifications, New Algorithm: RATTLE



Towards High-Accurate Predictions of Bulk Properties of Water

Motivation:

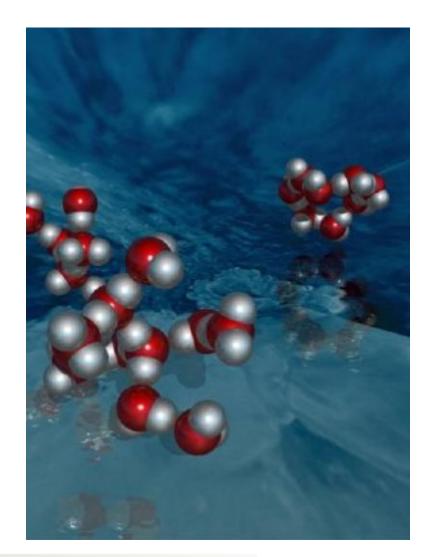
- the current state of theory and modeling of water is insufficient
- structure and dynamics of the H-bonding network in water has not been resolved

Model	Dipole	Dielectric	Self-	Average	Density	Expansion
	Moment	Constant	Diffusion,	Configurational	Maximum,	Coefficient,
			$10^{-5} \text{ cm}^2/\text{s}$	Energy, kJ/mol	$^{\circ}\mathrm{C}$	10-4 °C ⁻¹
TIP3P	2.35	82	5.19	-41.1	-91	9.2
TIP4P	2.18	52	3.29	-41.8	-25	4.4
Expt	2.95	78.4	2.30	-41.5	+3.984	2.53

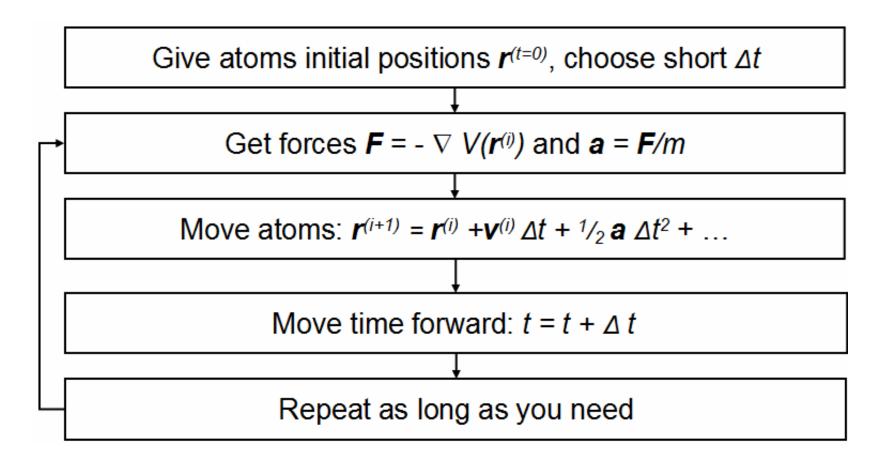
Towards High-Accurate Predictions of Bulk Properties of Water

Plan:

perform ab initio molecular dynamics simulations of water using FMO2-MP2 to provide a comprehensive and quantitative comparison with experimental results and to calibrate empirical potentials



Molecular Dynamics





Ab Initio Quantum Chemistry

Schrödinger Equation:

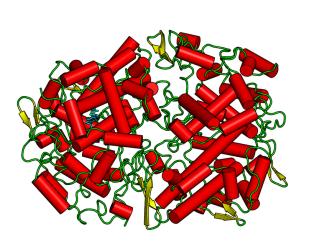
$$H_{e} \Psi_{\mu}(X;R) = E_{\mu}(R) \Psi_{\mu}(X;R)$$

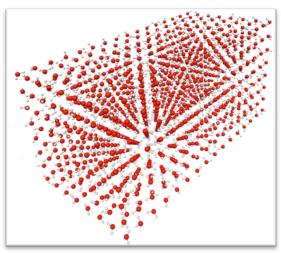
$$H_{e} = Z + V = \sum_{i=1}^{N} z(x_{i}) + \sum_{i>j=1}^{N} v(x_{i},x_{j})$$

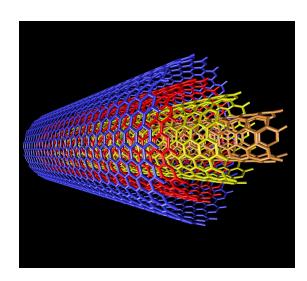
$$z(x_{i}) = \frac{1}{2} \Delta_{i} + \sum_{A=1}^{M} \frac{Z_{A}}{R_{A_{i}}}, \quad v(x_{i},x_{j}) = \frac{1}{r_{ij}}$$

Major Challenge of Modern Quantum Chemistry

 To apply to systems with thousands of correlated electrons and basis functions







Major Challenge of Modern Quantum Chemistry

- In order to make QM computationally tractable to large systems:
 - 1. Availability of supercomputers
 - 2. Development of novel and scalable methods (e.g. Fragment Molecular Orbital method)

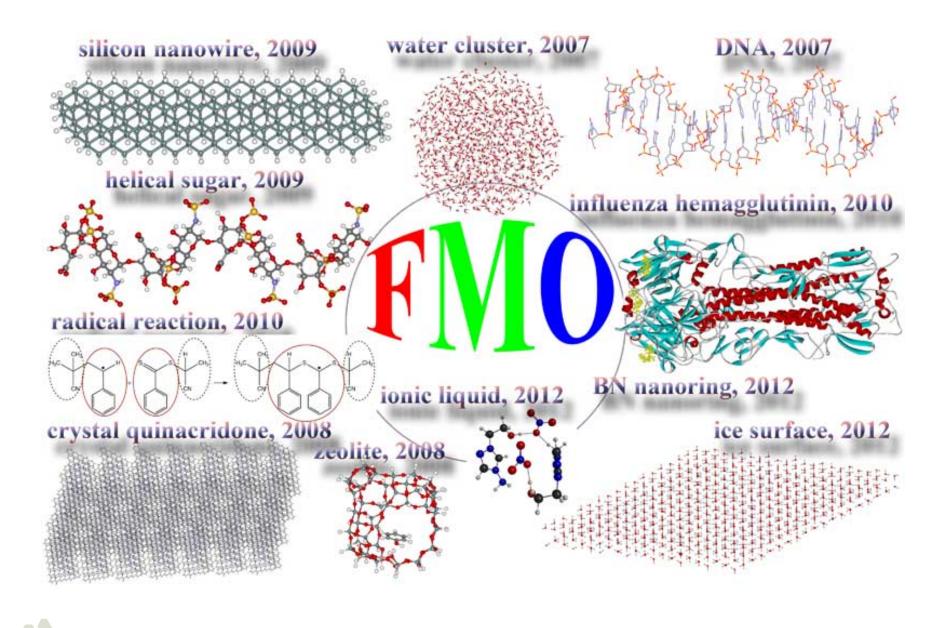


GAMESS

(General Atomic and Molecular Electronic Structure System)

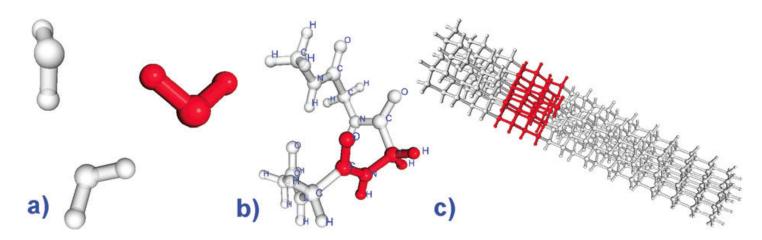
- Ab initio quantum chemistry package
- Maintained by the research group of Prof. Mark Gordon at Iowa State University
- Implemented all major quantum mechanical methods
 - Hartree- Fock
 - Møller Plesset perturbation theory
 - Coupled-cluster
 - Multiconfiguration consistent field
 - Configuration interaction
 - Density functional theory
- Ported to all major architectures
- Free and widely used on everything from laptops to supercomputers
- About a million lines of code, with an associated parallelization library comprising 15,000 lines
- Highly scalable, including many distributed data algorithms





Fragment Molecular Orbital, basics

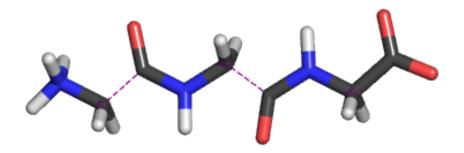
- FMO in GAMESS is due to Fedorov, Kitaura
- Split system into fragments and solve for the electronic structure of each fragment in the coulomb field of the whole system
- How? Quantum effects are short-range
 - Long-range interactions can be described by the coulomb operator (point charges)



Fragment Molecular Orbital, basics

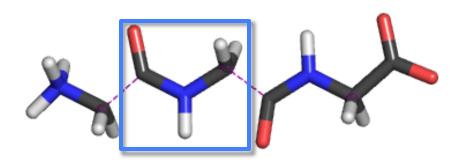
- Address major bottlenecks of quantum chemistry:
 Computational cost, memory, disc, bandwidth
- Main application to proteins (fragment: amino acid)
- Fully ab initio (no fitted parameters)
- Any QC method (MP2, MCSCF, CC, HF, DFT, ...)
- Linear cost
- Highly scalable (coarse, fine-grained parallelism)
- Pair Interaction Energy Decomposition Analysis (PIEDA): Electrostatic, Exchange Repulsion, Charge Transfer, Diffusion





$$E = \sum_{I}^{N} E_{I} + \sum_{I>J}^{N} (E_{IJ} - E_{I} - E_{J})$$
 $+ \sum_{I>J>K}^{N} \{ (E_{IJK} - E_{I} - E_{J} - E_{K}) - (E_{IJ} - E_{I} - E_{J}) - (E_{JK} - E_{J} - E_{K}) - (E_{KI} - E_{K} - E_{J}) \} + \cdots,$



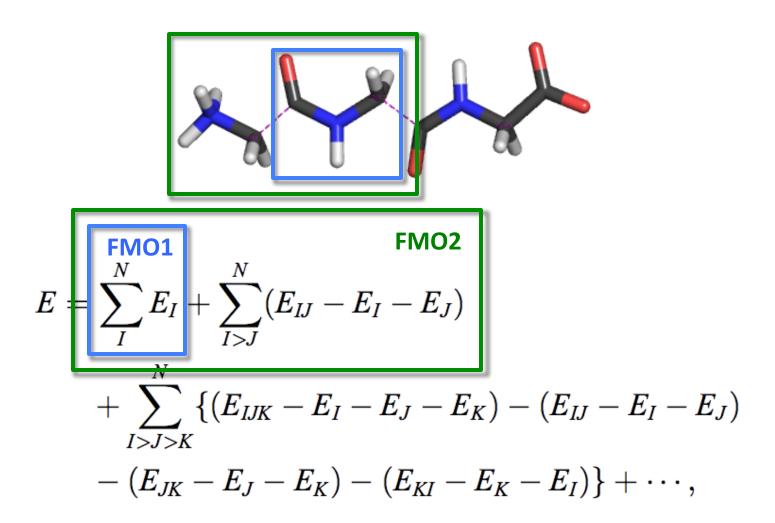


$$E = \sum_{I}^{FMO1} E_{I} + \sum_{I>J}^{N} (E_{IJ} - E_{I} - E_{J})$$

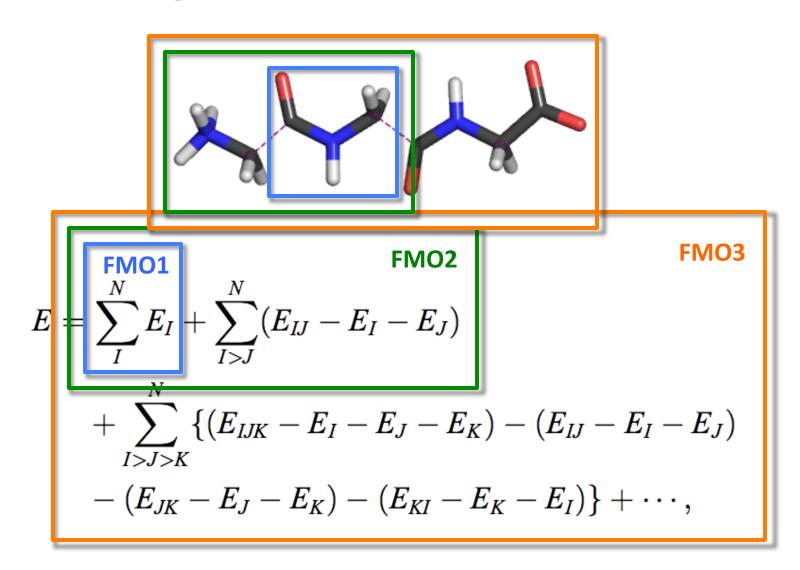
$$+ \sum_{I>J>K}^{N} \{ (E_{IJK} - E_{I} - E_{J} - E_{K}) - (E_{IJ} - E_{I} - E_{J})$$

$$- (E_{JK} - E_{J} - E_{K}) - (E_{KI} - E_{K} - E_{I}) \} + \cdots,$$



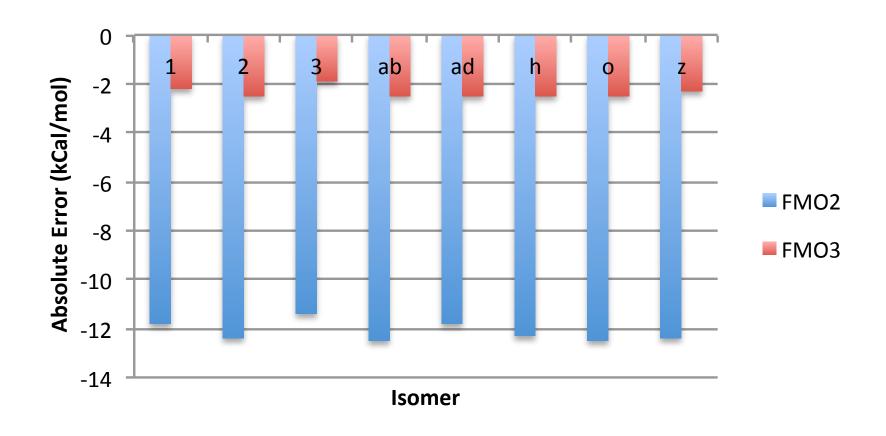








FMO 'Level' Accuracy



32 waters/FMO(2,3)/-MP2/6-31G*



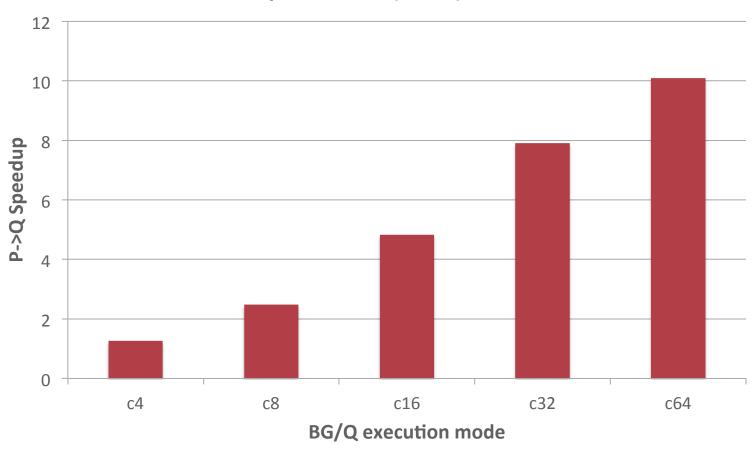
Porting GAMESS to Blue Gene/Q

- IBM XL compiler
- ESSL
- MPI-1



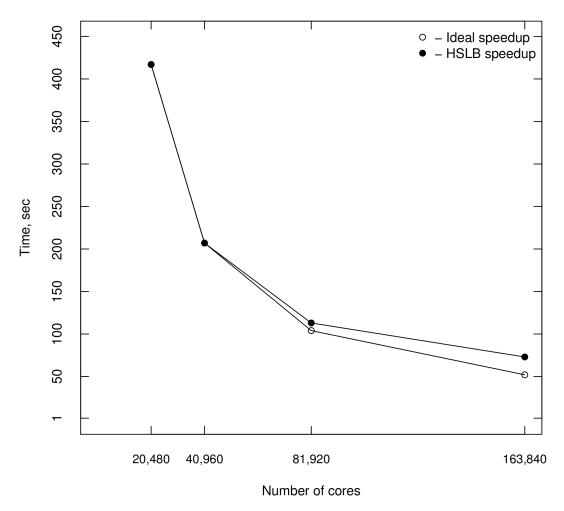
Performance on Mira

GAMESS speedup from BG/P(VN mode) to BG/Q benzoquinone/MP2(forces)/6-31G*



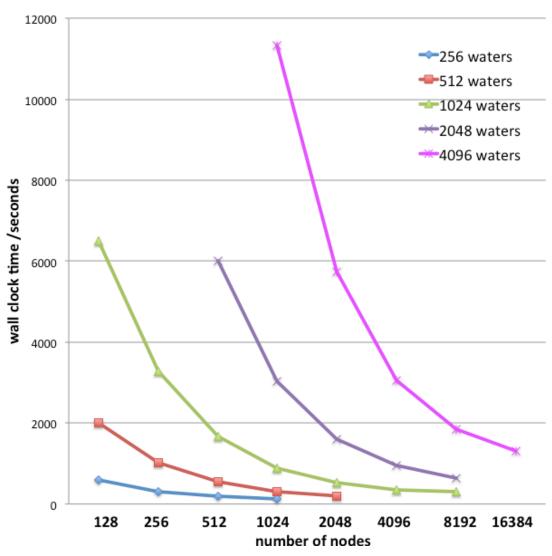
Scalability of FMO on Intrepid

Wall clock time for SCC iteration 1



COX-1 complexed with ibuprofen (17,767 atoms) using FMO2-RHF/6-31G*

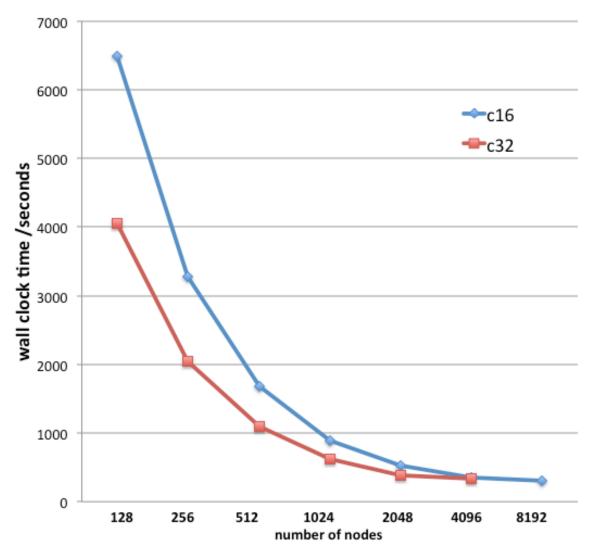
Scalability of FMO on Mira



FMO2-MP2(forces)/aug-cc-pvdz, c16 mode



Scalability of FMO on Mira



1024 waters/FMO2-MP2(forces)/aug-cc-pvdz



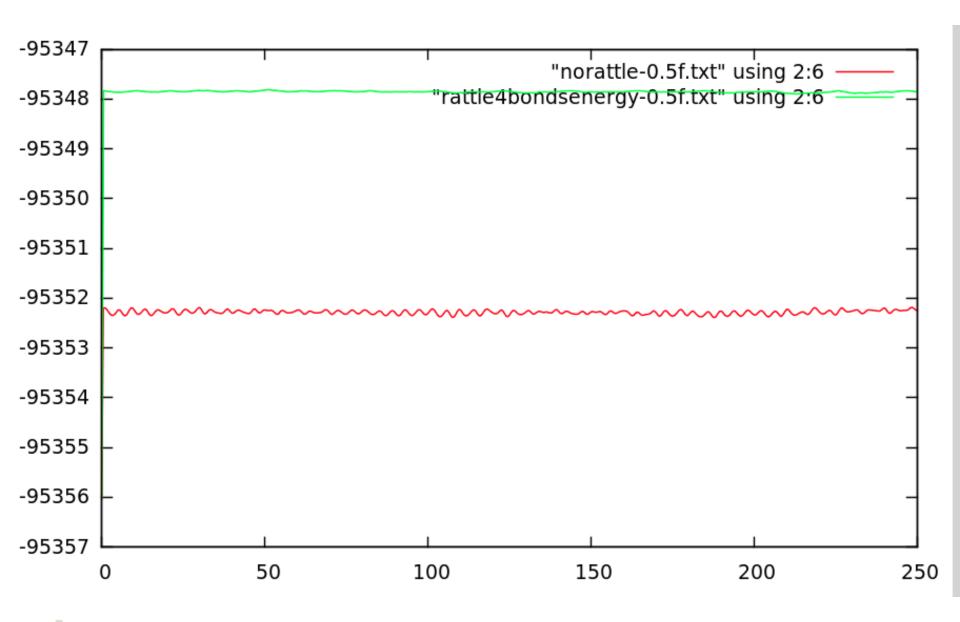
What is enabled by Mira over Intrepid

- This Early Science project focuses on bulk properties of water:
 - larger embedded clusters
 - longer dynamics simulations
 - higher levels of theory (accuracy)
 - larger basis sets

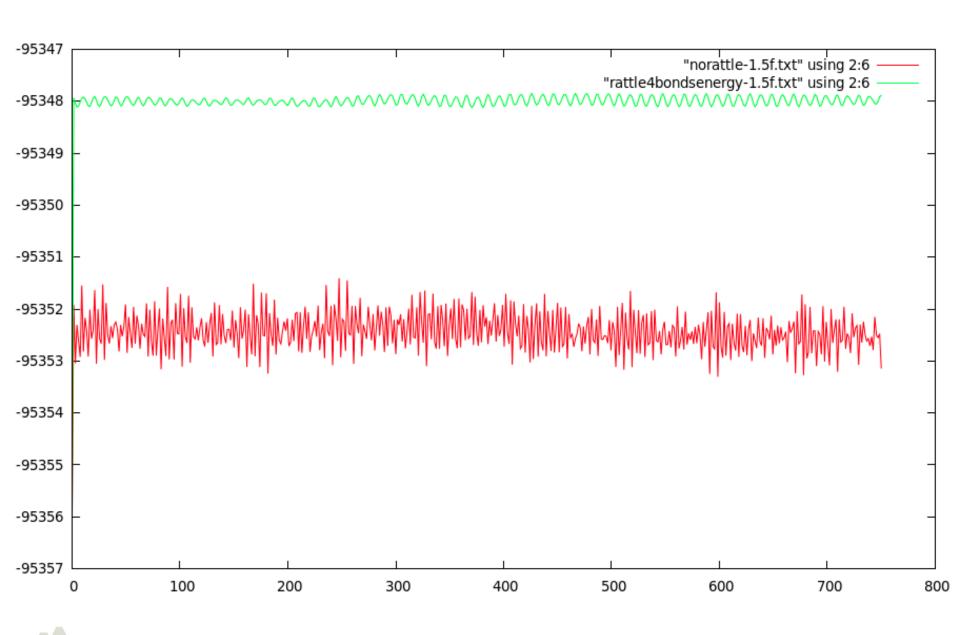
Code Modifications, New Algorithms: RATTLE

- A form of Constrained Dynamics to allow larger time steps and avoid local minima
- Constraints are applied to both distances and velocities simultaneously
- Lagrange-multiplier based method developed especially for velocity version of Verlet integrators
- Helps the trajectory to sample the most important regions of phase space
- Improves the stability of the trajectory by removing abrupt shifts in molecule positions









Summary

- Successfully ported GAMESS on Blue Gene/Q systems
- Successfully ran test and benchmark calculation on Intrepid and Blue Gene/Q systems
 - Relative node-to-node speedup of up to 10x
- Demonstrated scalability and performance of FMO
 - Scales up to 16 racks of Mira
- Implemented a new functionality on GAMESS (RATTLE algorithm) which would significantly reduce the computational cost of the project



Acknowledgment

- This research used resources of the Argonne Leadership Computing Facility at Argonne National Laboratory, which is supported by the Office of Science of the U.S. Department of Energy under contract DE-ACO2-06CH11357.
- ALCF's Early Science Program